



- 60    tgaaaagatagaataaaatggcctcgtg

1       ATGGCGCGGCCAGCGCTGCTGGGCGAG  
1       M   A   R   P   A   L   L   G   E

61       GGCCAAGTTGCCGCGGCCACAGAAGTT  
21       G   Q   V   A   A   A   T   E   V

121      GAAAATCTCTGCACGATAATATGGACG  
41       E   N   L   C   T   I   I   W   T

181      ACTCTCAGATATTTTAGTCACTTTGAT  
61       T   L   R   Y   F   S   H   F   D

241      CATCGTAAAGAGGAATTACCCCTGGAT  
81       H   R   K   E   E   L   P   L   D

301      AGTGCCAATGAAAGTGAGAAGCCTAGC  
101      S   A   N   E   S   E   K   P   S

361      GGTGATCCTGAGTCCGCTGTGACTGAG  
121      G   D   P   E   S   A   V   T   E

421      AAGTG TTCCTGGCTCCCTGGAAGGAAT  
141      K   C   S   W   L   P   G   R   N

Fig. 1A

ccgaattcgggcacgagccgagggcgaggggcctgc

CTGTTGGTGCTGCTACTGTGGACCGCCACCGTG

L L V L L L W T A T V

CAGCCACCTGTGACGAATTTGAGCGTCTCTGTC

Q P P V T N L S V S V

TGGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC

W S P P E G A S P N C

GACCAACAGGATAAGAAAATTGCTCCAGAAACT

D Q Q D K K I A P E T

GAGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT

E K I C L Q V G S Q C

CCTTTGGTGAAAAAGTGCATCTCACCCCCTGAA

P L V K K C I S P P E

CTCAAGTGCATTTGGCATAACCTGAGCTATATG

L K C I W H N L S Y M

ACAAGCCCTGACACACACTATACTCTGTACTAT

T S P D T H Y T L Y Y

*Fig. 1B*

481	TGGTACAGCAGCCTGGACAAAAGTCGT
161	W Y S S L E K S R
541	ATTGCTTGTTTCCTTTAAATTGACTAAA
181	I A C S F K L T K
601	ATAATGGTCAAGGATAATGCTGGGAAA
201	I M V K D N A G K
661	TCCTATGTGAAACCTGATCCTCCACAT
221	S Y V K P D P P H
721	TTAGTGCAGTGGAAGAATCCACAAAAT
241	L V Q W K N P Q N
781	GTCAATAATACTCAAACCGACCGACAT
261	V N N T Q T D R H
841	AATTCCGAATCTGATAGAAACATGGAG
281	N S E S D R N M E
901	GCCGACGCTGTCTACACAGTCAGAGTA
301	A D A V Y T V R V
961	AACAAACTGTGGAGTGATTGGAGTGAA
321	N K L W S D W S E

*Fig. 1C*

CAATGTGAAAACATCTATAGAGAAGGTCAACAC  
Q C E N I Y R E G Q H

GTGGAACCTAGTTTTGAACATCAGAACGTTCAA  
V E P S F E H Q N V Q

ATTAGGCCATCCTGCAAAATAGTGTCTTTAACT  
I R P S C K I V S L T

ATTAAACATCTTCTCCTCAAAAATGGTGCCTTA  
I K H L L L K N G A L

TTAGAAGCAGATGCTTAACTTATGAAGTGGAG  
F R S R C L T Y E V E

AATATTTTAGAGGTTGAAGAGGACAAATGCCAG  
N I L E V E E D K C Q

GGTACAAGTTGTTTCCAACCTCCCTGGTGTTCTT  
G T S C F Q L P G V L

AGAGTCAAAACAAACAAGTTATGCTTTGATGAC  
R V K T N K L C F D D

GCACAGAGTATAGGTAAGGAGCAAAACTCCACC  
A Q S I G K E Q N S T

*Fig. 1D*

1021	<u>TTCTACACCACCATGTTACTCACCATT</u>
341	<u>F Y T T M L L T I</u>
1081	<u>CTTTTTTACCTGAAAAGGCTTAAGATC</u>
361	<u>L F Y L K R L K I</u>
1141	ATTTTAAAGAAATGTTTGGAGACCAG
381	I F K E M F G D Q
1201	ATCTATGAGAAACAATCCAAAGAAGAA
401	I Y E K Q S K E E
1261	AAAGCAGCTCCTTGAtgggggagaagtg
421	K A A P *
1321	gatttattgcattctccatttggtatc
1381	cttgaaaaacaggcagctcctaagagc
1441	ccaaacccaaaggagctccttccaaga
1501	ccctaaaagcagatgttttgccaaatc
1561	accatcaattcatctaatacaggaattg

*Fig. 1E*

CCAGTCCTTTGTCGCAGTGGCAGTCATAATCCTC  
P V F V A V A V I I L

ATTATATTTCTCCAATTCCTGATCCTGGCAAG  
I I F P P I P D P G K

AATGATGATACCCTGCACTGGAAGAAGTATGAC  
N D D T L H W K K Y D

ACGGATTCTGTAGTGCTGATAGAAAACCTGAAG  
T D S V V L I E N L K

atttcttttcttgccttcaatgtgaccctgtgaa

tgggggacttggttaaatagaaactgaaactact  
cacaggtcttgatgtgacttttgcattgaaaac  
aaagcaagagttcttctcgttccttgttccaat  
cccaaactagaggacaaagacagggggacaatg  
tgatggcttcctaaggaatctctgcttgctctg

*Fig. 1F*

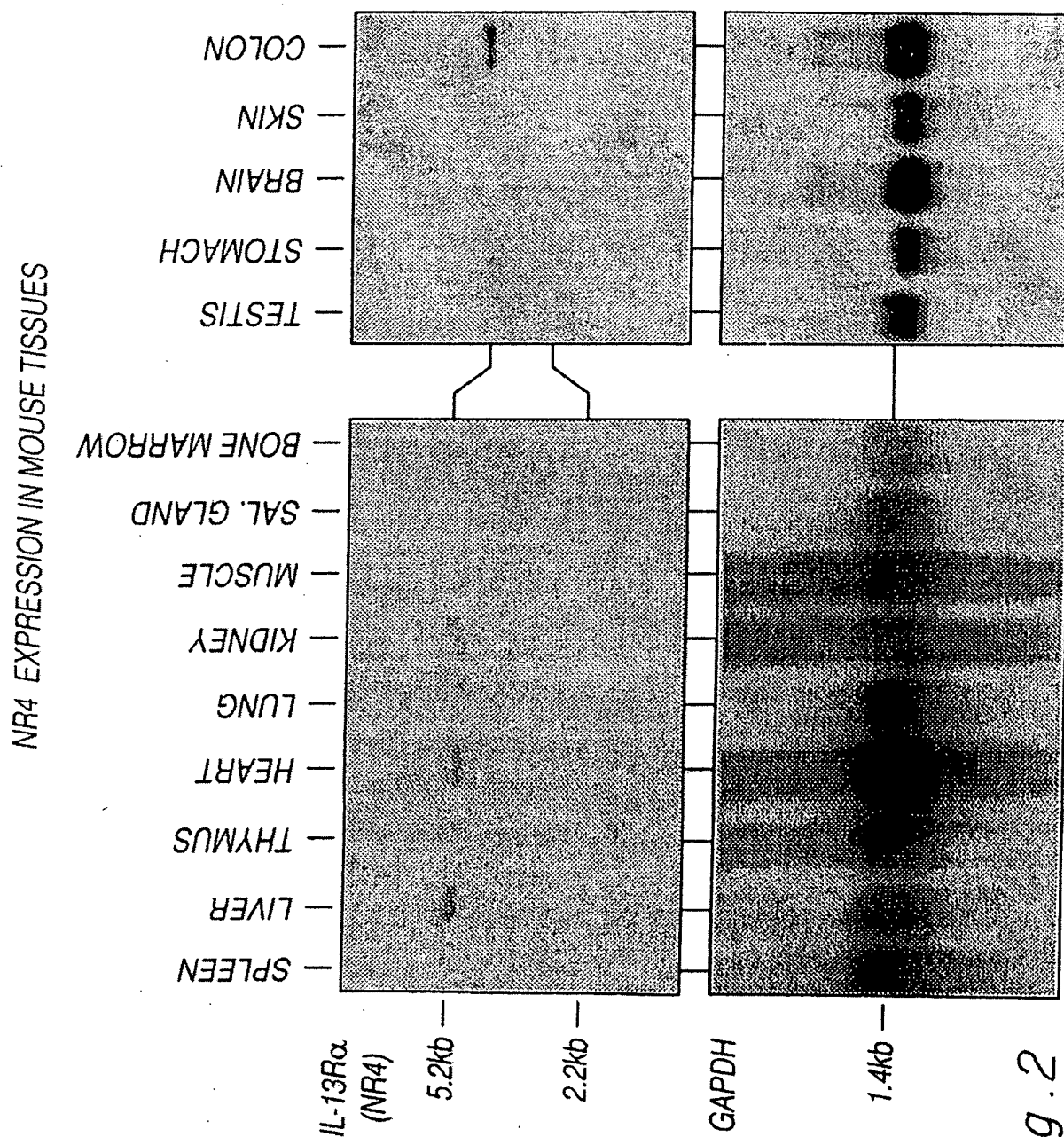
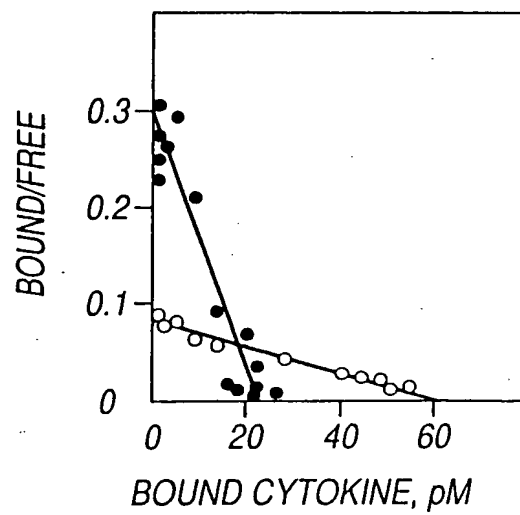
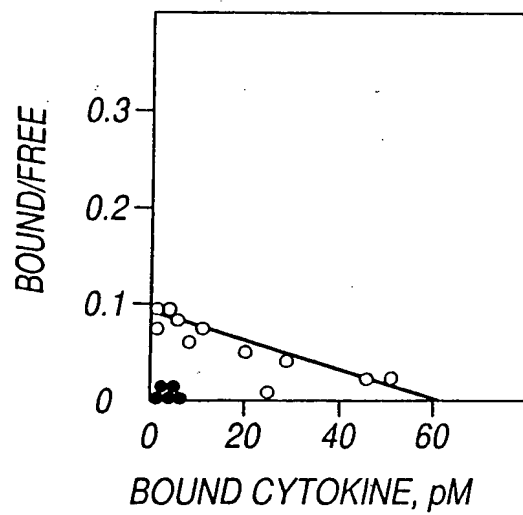
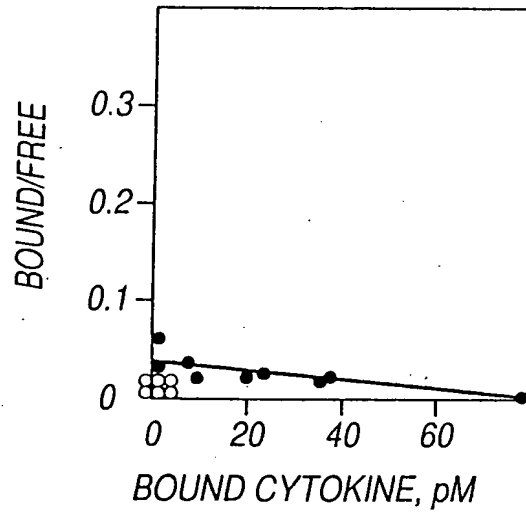


Fig. 2





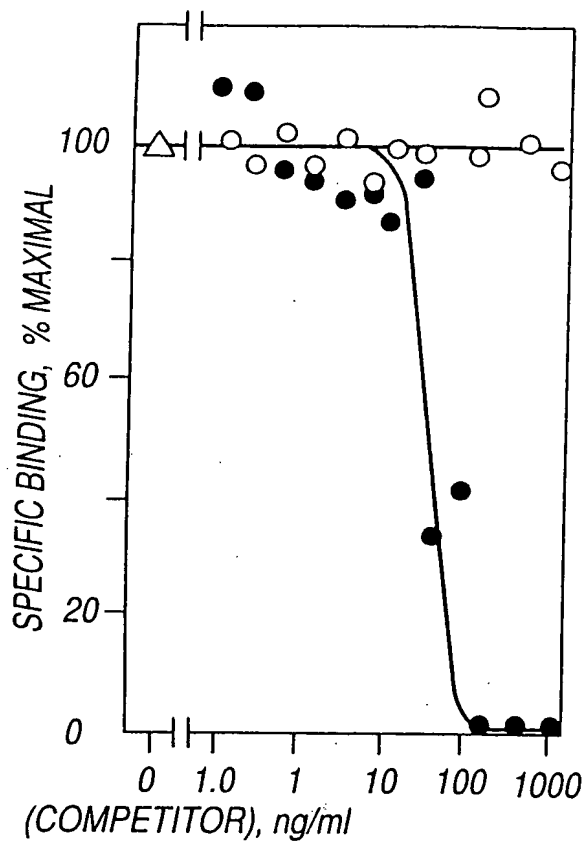


Fig. 4A

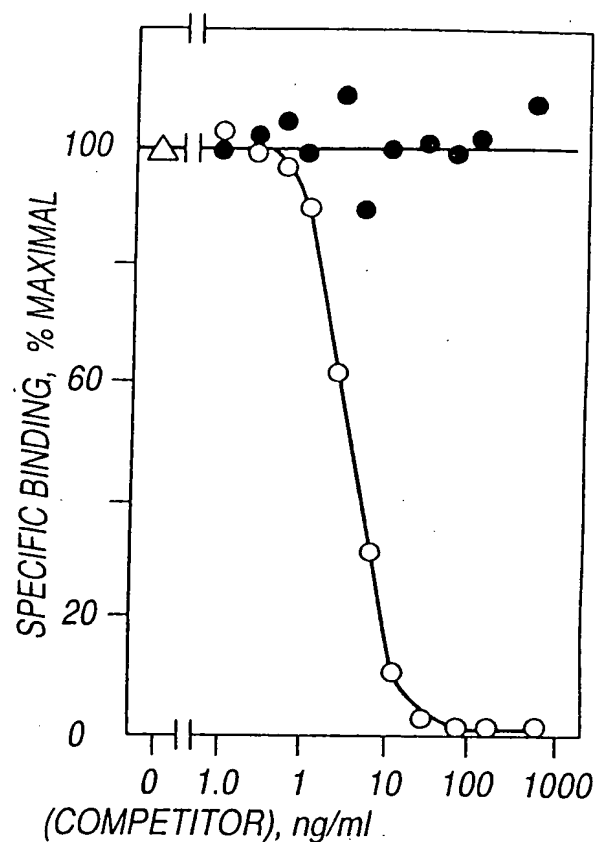


Fig. 4B

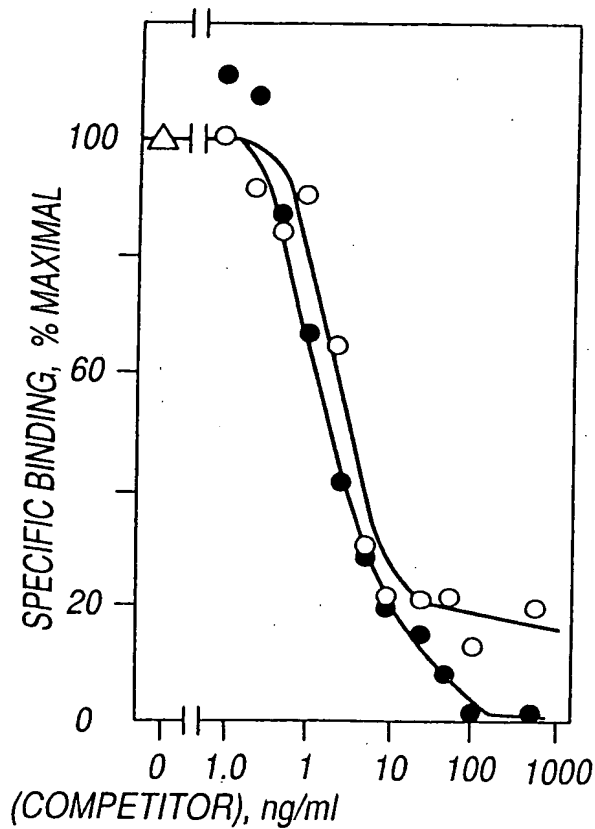


Fig. 4C

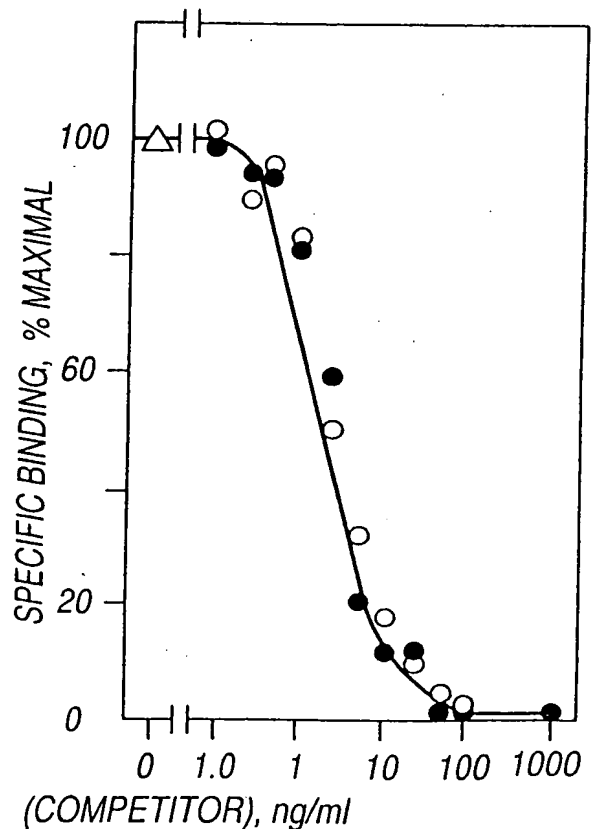
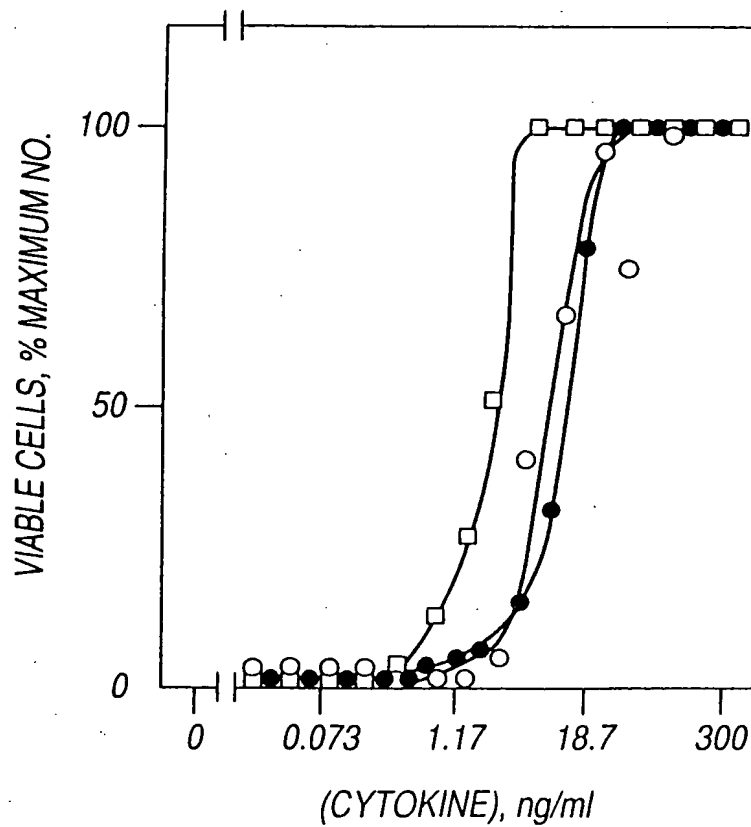
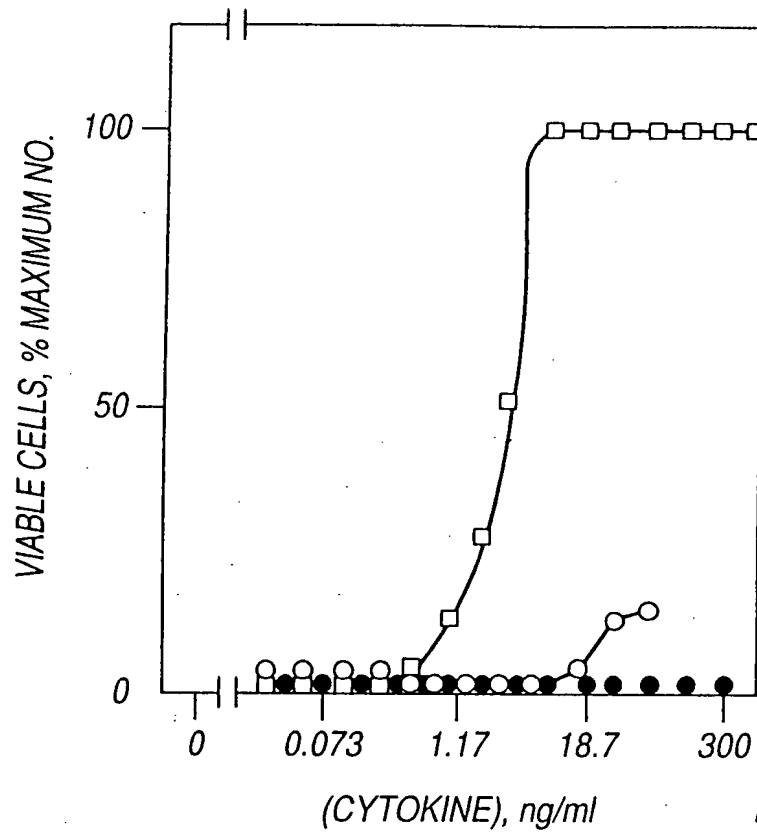


Fig. 4D



CROSS-SPECIES CONSERVATION OF THE NR-4 (IL-13R  $\alpha$ )  
 GENE

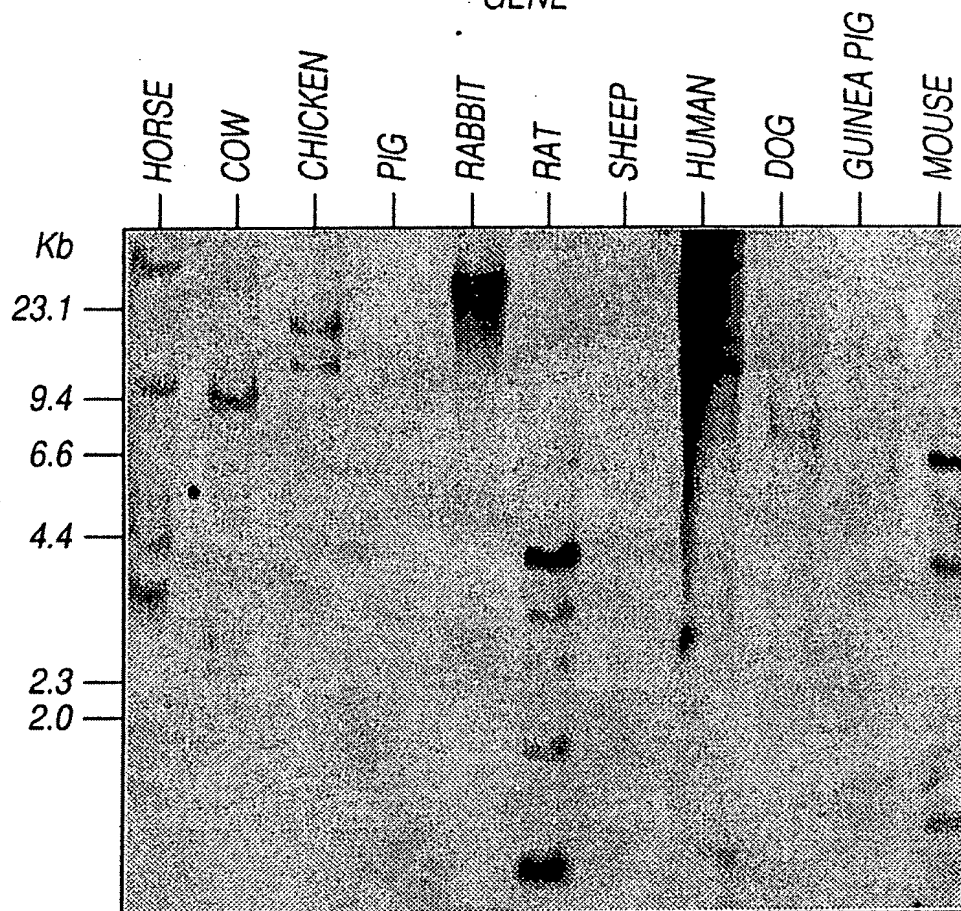


Fig. 6

(major)

DYKDD	DDYKD	DDESR	TEVQP	PVTXL	SV
1	5	10	15	20	25

(minor)

ASISS	SDYKD	DDESR	TEVQP	PVTXL	SV
1	5	10	15	20	25

Fig. 10

H		gagtctaacacggaccaaggagtttaac
M	-60	tgaaaagatagaataaatggcctcgtgc
H		M E W P A R L C G
		ATGGAGTGGCCGGCGCGGCTCTGCGGGC
		* * * *
M	1	ATGGCGCGGCCAGCGCTGCTGGGCGAGC
M	1	M A R P A L L G E
H		G G G G A P T E T
H		GGGGGCGGGGGCGCGCCTACGGAAACTC
		* * * *
M	61	GGCCAAGTTGCCGCGGCCACAGAAGTTC
M	21	G Q V A A A T E V
H		E N L C T V I W T
H		GAAAACCTCTGCACAGTAATATGGACAT
		* * * * *
M	121	GAAAATCTCTGCACGATAATATGGACGT
M	41	E N L C T I I W T
H		S L W Y F S H F G
H		AGTCTATGGTATTTTAGTCATTTTGGCG
		* * * * *
M	181	ACTCTCAGATATTTTAGTCACTTTGATG
M	61	T L R Y F S H F D

Fig. 7A

acgtgcgggccggggttccgagggcgagaggctgc

.....

cgaattcggcacgagccgagggcgagggcctgc

L W A L L L C A G G G G  
TGTGGGCGCTGCTGCTCTGCGCCGGCGGGGGGC  
\* \* \* \*

TGTTGGTGCTGCTACTGTGGACCGCCACCGTG - - -  
L L V L L L W T A T V -

Q P P V T N L S V S V  
AGCCACCTGTGACAAATTTGAGTGTCTCTGTT  
\* \* \* \* \* \* \* \* \* \*

AGCCACCTGTGACGAATTTGAGCGTCTCTGTC  
Q P P V T N L S V S V

W N P P E G A S S N C  
GGAATCCACCCGAGGGAGCCAGCTCAAATTGT  
\* \* \* \* \* \* \* \* \*

GGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC  
W S P P E G A S P N C

D K Q D K K I A P E T  
ACAAACAAGATAAGAAAATAGCTCCGGAAACT  
\* \* \* \* \* \* \* \* \*

ACCAACAGGATAAGAAAATTGCTCCAGAAACT  
D Q Q D K K I A P E T

*Fig. 7B*

H		R	R	S	I	E	V	P	L	N																			
H		C	G	T	C	G	T	T	C	A	T	A	G	A	A	G	T	A	C	C	C	T	G	A	A	T	G		
			*			*		*	*																				
M	241	C	A	T	C	G	T	A	A	G	A	G	G	A	A	T	T	A	C	C	C	C	T	G	G	A	T	G	
M	81	H	R	K	E	E	L	P	L	D																			
H		S	T	N	E	S	E	K	P	S																			
H		A	G	C	A	C	A	A	T	G	A	G	A	G	T	G	A	G	A	A	G	C	C	T	A	G	C	A	
		*		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	
M	301	A	G	T	G	C	C	A	A	T	G	A	A	A	G	T	G	A	G	A	A	G	C	C	T	A	G	C	C
M	101	S	A	N	E	S	E	K	P	S																			
H		G	D	P	E	S	A	V	T	E																			
H		G	G	T	G	A	T	C	C	T	G	A	G	T	C	T	G	C	T	G	T	G	A	C	T	G	A	A	C
		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	
M	361	G	G	T	G	A	T	C	C	T	G	A	G	T	C	C	G	C	T	G	T	G	A	C	T	G	A	G	C
M	121	G	D	P	E	S	A	V	T	E																			
H		K	C	S	W	L	P	G	R	N																			
H		A	A	G	T	G	T	T	C	T	T	G	G	C	T	C	C	C	T	G	G	A	A	G	G	A	A	T	A
		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	
M	421	A	A	G	T	G	T	T	C	C	T	T	G	G	C	T	C	C	C	T	G	G	A	A	G	G	A	A	T
M	141	K	C	S	W	L	P	G	R	N																			
H		W	H	R	S	L	E	K	I	H																			
H		T	G	G	C	A	C	A	A	G	C	C	T	G	G	A	A	A	A	A	A	A	T	T	C	A	T	C	

Fig.7C

E R I C L Q V G S Q C  
AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT

\* \* \* \* \*

AGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT  
E K I C L Q V G S Q C

I L V E K C I S P P E  
TTTTGGTTGAAAAATGCATCTCACCCCCAGAA

\* \* \* \* \*

CTTTGGTGAAAAAGTGCATCTCACCCCCTGAA  
P L V K K C I S P P E

L Q C I W H N L S Y M  
TTCAATGCATTTGGCACAACCTGAGCTACATG

\* \* \* \* \*

TCAAGTGCATTTGGCATAACCTGAGCTATATG  
L K C I W H N L S Y M

T S P D T N Y T L Y Y  
CCAGTCCCGACACTAATACTCTCTACTAT

\* \* \* \* \*

CAAGCCCTGACACACTATACTCTGTACTAT  
T S P D T H Y T L Y Y

Q C E N I F R E G Q Y  
AATGTGAAAACATCTTTAGAGAAGGCCAATAC

*Fig. 7D*

			*		*	*	*	*	
M	481	TGGTACAGCAGCCTGGAGAAAAGTCGTC							
M	161	W Y S S L E K S R							
H		F G C S F D L T K							
H		TTTGGTTGTTTCCTTTGATCTGACCAAAG							
			*	*	*		*	*	*
M	541	ATTGCTTGTTTCCTTTAAATTGACTAAAG							
M	181	I A C S F K L T K							
H		Q I M V K D N A G							
H		CAAATAATGGTCAAGGATAATGCAGGAA							
			*	*	*	*	*	*	*
M	601	CAAATAATGGTCAAGGATAATGCTGGGA							
M	201	Q I M V K D N A G							
H		T S R V K P D P P							
H		ACTTCCCGTGTGAAACCTGATCCTCCAC							
			*	*		*	*	*	*
M	661	ACTTCCTATGTGAAACCTGATCCTCCAC							
M	221	T S Y V K P D P P							
H		L Y V Q W E N P Q							
H		CTATATGTGCAATGGGAGAATCCACAGA							
			*	*	*	*	*	*	*
M	721	TTATTAGTGCAGTGGGAAGAATCCACAAA							
M	241	L L V Q W K N P Q							

Fig. 7E



\* \* \* \* \* \* \* \* \*  
AATGTGAAAACATCTATAGAGAAGGTCAACAC  
Q C E N I Y R E G Q H  
  
V K D S S F E Q H S V  
TGAAGGATTCCAGTTTTGAACAACACAGTGTC  
\* \* \* \* \*  
TGGAACCT - - - AGTTTTGAACATCAGAACG TT  
V E P - S F E H Q N V  
  
K I K P S F N I V P L  
AAATTAAACCATCCTTCAATATAGTGCCTTTA  
\* \* \* \* \*  
AAATTAGGCCATCCTGCAAAATAGTGTCTTTA  
K I R P S C K I V S L  
  
H I K N L S F H N D D  
ATATTAAAAACCTCTCCTTCCACAATGATGAC  
\* \* \* \* \*  
ATATTAAACATCTTCTCCTCAAAAATGGTGCC  
H I K H L L L K N G A  
  
N F I S R C L F Y E V  
ATTTTATTAGCAGATGCCTATTTTATGAAGTA  
\* \* \* \* \*  
ATTTTAGAAGCAGATGCTTAACCTTATGAAGTG  
N F R S R C L T Y E V

Fig. 7F

H		E	V	N	N	S	Q	T	E	T
H		GAAGTCAATAACAGCCAAACTGAGACAC								
		*	*	*	*		*	*		
M	781	GAGGTCAATAATACTCAAACCGACCGAC								
M	261	E	V	N	N	T	Q	T	D	R
H		E	N	P	E	F	E	R	N	V
H		GAGAATCCAGAATTTGAGAGAAATGTGG								
		*		*			*	*		
M	841	CAGAATTCCGAATCTGATAGAAACATGG								
M	281	Q	N	S	E	S	D	R	N	M
H		L	P	D	T	L	N	T	V	R
H		CTTCCTGATACTTTGAACACAGTCAGAA								
		*		*			*	*	*	
M	901	CTTGCCGACGCTGTCTACACAGTCAGAG								
M	301	L	A	D	A	V	Y	T	V	R
H		D	D	K	L	W	S	N	W	S
H		GATGACAAACTCTGGAGTAATTGGAGCC								
		*		*	*	*	*		*	*
M	961	GACAACAAACTGTGGAGTGATTGGAGTG								
M	321	D	N	K	L	W	S	D	W	S
H		T	L	Y	I	T	M	L	L	I
H		ACACTCTACATAACCATGTTACTCATTG								

*Fig. 7G*

H N V F Y V Q E A K C  
ATAATGTTTTCTACGTCCAAGAGGCTAAATGT  
\* \* \* \* \*  
ATAATATTTTAGAGGTTGAAGAGGACAAATGC  
H N I L E V E E D K C  
  
E N T S C F M V P G V  
AGAATACATCTTGTTTCATGGTCCCTGGTGTT  
\* \* \* \* \*  
AGGGTACAAGTTGTTTCCAACCTCCCTGGTGTT  
E G T S C F Q L P G V  
  
I R V K T N K L C Y E  
TAAGAGTCAAAACAAATAAGTTATGCTATGAG  
\* \* \* \* \*  
TAAGAGTCAAAACAAACAAGTTATGCTTTGAT  
V R V K T N K L C F D  
  
Q E M S I G K K R N S  
AAGAAATGAGTATAGGTAAGAAGCGCAATTCC  
\* \* \* \* \*  
AAGCACAGAGTATAGGTAAGGAGCAAAACTCC  
E A Q S I G K E Q N S  
  
V P V I V A G A I I V  
TTCCAGTCATCGTCGCAGGTGCAATCATAGTA

*Fig. 7H*

			*		*		*		*		*		*
M	1021	ACCTTCTACACCACCATGTTACTCACCA											
M	341	T F Y T T M L L T											
H		L L L Y L K R L K											
H		CTCCTGCTTTACCTAAAAAGGCTCAAGA											
			*	*		*	*	*	*	*	*	*	*
M	1081	CTCCTTTTTTTACCTGAAAAGGCTTAAGA											
M	361	L L F Y L K R L K											
H		K I F K E M F G D											
H		AAGATTTTTTAAAGAAATGTTTGGAGACC											
			*	*	*	*	*	*	*	*	*	*	*
M	1141	AAGATTTTTTAAAGAAATGTTTGGAGACC											
M	381	K I F K E M F G D											
H		D I Y E K Q T K E											
H		GACATCTATGAGAAGCAAACCAAGGAGG											
			*	*	*	*	*	*	*	*	*	*	*
M	1201	GACATCTATGAGAAACAATCCAAAGAAG											
M	401	D I Y E K Q S K E											
H		K K A S Q *											
H		AAGAAAGCCTCTCAGTGAtggagataat											
			*	*	*								
M	1261	AAGAAAGCAGCTCCTTGAtgggggagaag											
M	421	K K A A P *											

Fig. 7I

\* \* \* \* \*

TTCCAGTCTTTGTCGCAGTGGCAGTCATAATC  
I P V F V A V A V I I

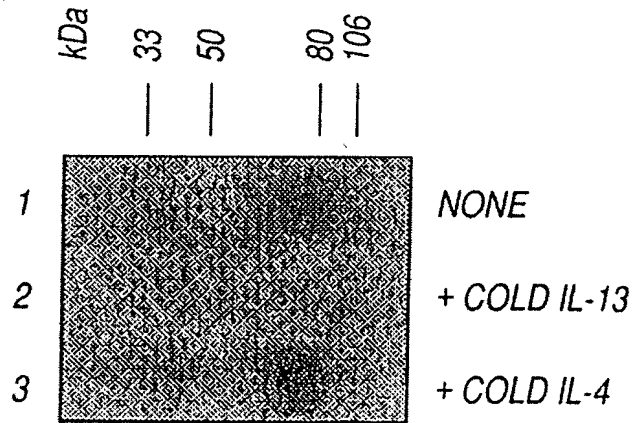
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\* \* \* \* \*  
TCATTATATTTCTCCAATTCCTGATCCTGGC  
I I I F P P I P D P G

Q N D D T L H W K K Y  
AGAATGATGATACTCTGCACTGGAAGAAGTAC  
\* \* \* \* \*  
AGAATGATGATACCCTGCACTGGAAGAAGTAT  
Q N D D T L H W K K Y

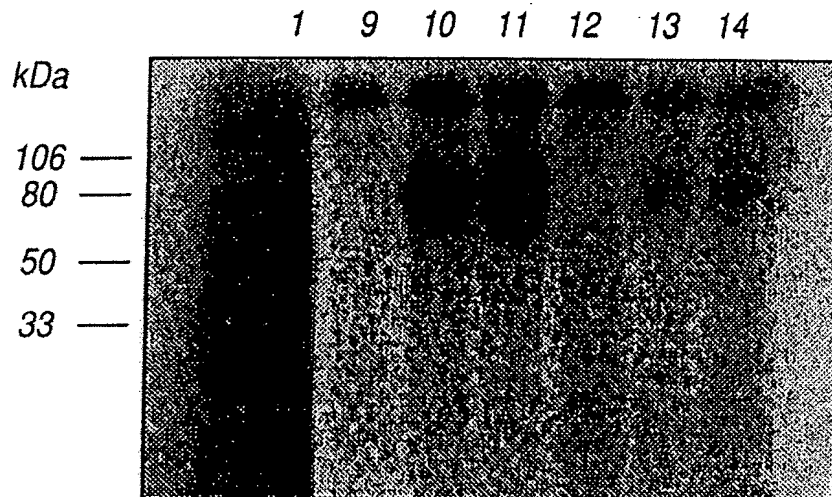
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AAACCGACTCTGTAGTGCTGATAGAAAACCTG  
\* \* \* \* \*  
AAACGGATTCTGTAGTGCTGATAGAAAACCTG  
E T D S V V L I E N L

ttatttttaccttcactgtgaccttgagaaga  
tgatttctttcttgccttcaatgtgaccctgt

*Fig.7J*



*Fig.8*



*Fig.9*